24348-501NATL.ST25
SEQUENCE LISTING

<110>   Ben-Sasson, Shmuel A.
        Cohen, Einat

<120>   Amino Acid Sequences Capable of Facilitating Penetration Across a
        Biological Barrier

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<140>   US 10/501,838
<141>   2003-02-07

<150>   PCT/IB03/00968
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Asn Xaa


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<220>
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<400> 41

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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<210> 42
<211> 25
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<220>
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<223>  Wherein Xaa is any amino acid

<220>
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<222>  (25)..(25)
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<400>  42

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa         .
            20              25


<210>  43
<211>  23
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<213>  Artificial

<220>
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<400>  43

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1                   5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20
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<223> Wherein Xaa is a hydrophobic amino acid

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<220>
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<223> Wherein Xaa is a hydrophobic amino acid

<400> 44

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20

<210> 45
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<223> Wherein Xaa is any amino acid

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<223> Wherein Xaa is a hydrophobic amino acid

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<223> Wherein Xaa is a charged amino acid

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<223> Wherein Xaa is any amino acid

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<222> (21)..(21)
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<223> Wherein Xaa is any amino acid

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<223> Wherein Xaa is a hydrophobic amino acid

<400> 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20

<210> 46
<211> 24
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<220>
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<220>

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<222>  (12)..(12)
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<223>  Wherein Xaa is a hydrophobic amino acid

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<220>
<221>  VARIANT
<222>  (24)..(24)
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<400> 46

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20

<210> 47
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<223> wherein Xaa is any amino acid

<400> 47

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25

<210> 48
<211> 23
<212> PRT
<213> Artificial

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<220>
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<223> wherein Xaa is a charged amino acid

<220>
<221> VARIANT
<222> (3)..(3)
<223> wherein Xaa is any amino acid

<220>
<221> VARIANT
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<223> wherein Xaa is a hydrophobic amino acid

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<223> wherein Xaa is a charged amino acid

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<223> wherein Xaa is any amino acid

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<221> VARIANT
<222> (9)..(12)
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<221> VARIANT
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<221> VARIANT
<222> (14)..(14)
<223> wherein Xaa is a hydrophobic amino acid

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<221> VARIANT
<222> (15)..(16)
<223> wherein Xaa is any amino acid

<220>
<221> VARIANT
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<222> (19)..(19)
<223> wherein Xaa is any amino acid

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<400>  48

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1                   5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20


<210>  49
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<213>  Artificial

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<223> Wherein Xaa is a hydrophobic amino acid

<400> 49

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20
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<210> 50
<211> 26
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<213> Artificial

<220>
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<223> Wherein Xaa is any amino acid

<220>
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<223> Wherein Xaa is any amino acid, or no amino acid is present

<220>
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       present

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<223>  wherein Xaa is any amino acid, or is not present

<220>
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<223>  wherein Xaa is a hydrophobic amino acid, or is not present

<220>
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<220>
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<223>  Wherein Xaa is a hydrophobic amino acid

<400>  50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25


<210>  51
<211>  28
<212>  PRT
<213>  Artificial

<220>
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<223>  Wherein Xaa is a charged amino acid

<220>
<221>  VARIANT
<222>  (4)..(6)
<223>  Wherein Xaa is any amino acid

<220>
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<222>  (7)..(7)
<223>  Wherein Xaa is a charged amino acid

<220>
<221>  VARIANT
<222>  (8)..(8)
<223>  Wherein Xaa is a hydrophobic amino acid

<220>
<221>  VARIANT
<222>  (9)..(9)
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<223> wherein Xaa is a hydrophobic amino acid, or not present

<220>
<221> VARIANT
<222> (10)..(10)
<223> wherein Xaa is any amino acid, or is not present

<220>
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<221> VARIANT
<222> (15)..(15)
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<220>
<221> VARIANT
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<222> (17)..(18)
<223> wherein Xaa is any amino acid

<220>
<221> VARIANT
<222> (19)..(19)
<223> wherein Xaa is any amino acid, or is not present

<220>
<221> VARIANT
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<223> wherein Xaa is a hydrophobic amino acid

<220>
<221> VARIANT
<222> (21)..(21)
<223> wherein Xaa is a hydrophobic amino acid, or is not present

<220>
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<223> wherein Xaa is a charged amino acid

<220>
<221> VARIANT
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<220>
<221> VARIANT
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<220>
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<222> (27)..(28)
<223> wherein Xaa is a hydrophobic amino acid

<400> 51

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20   25


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<210>  52
<211>  23
<212>  PRT
<213>  Artificial

<220>
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<221>  misc_feature
<222>  (1)..(23)
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<220>
<221>  VARIANT
<222>  (4)..(4)
<223>  Wherein Xaa is a charged amino acid

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<221>  VARIANT
<222>  (5)..(10)
<223>  Wherein Xaa is a hydrophobic amino acid

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<221>  VARIANT
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<223>  Wherein Xaa is any amino acid

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<221>  VARIANT
<222>  (16)..(16)
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<220>
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<222>  (17)..(17)
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<220>
<221> VARIANT
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<223> Wherein Xaa is a hydrophobic amino acid

<400> 52

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1   5   10   15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                20

<210> 53
<211> 205
<212> PRT
<213> Artificial

<220>
<223> Penetrating peptide consensus sequence

<400> 53

Met Lys Asn Tyr His Asp Ile Val Leu Ala Leu Ala Gly Val Cys Gln
1   5   10   15

Ser Ala Lys Leu Val His Gln Leu Ala Thr Glu Ser Arg Ala Asp Ser
                20   25   30

Glu Thr Phe Leu Thr Ala Leu Asn Ser Leu Phe Ile Thr Gln Pro Gln
                35   40   45

Arg Ile Glu Asp Val Phe Gly Gly Glu Val Arg His Leu Lys Leu Gly
    50   55   60

Leu Glu Thr Leu Ile His Gln Leu Asn Ala Gln Gly Asp Gln Asn Leu
65   70   75   80

Thr Arg Tyr Trp Leu Ser Leu Leu Ala Leu Glu Gly Lys Leu Ser Lys
                85   90   95

Asn Ser Asp Ala Lys Gln Thr Leu Gly Asn Arg Ile Ser Arg Leu Lys
                100   105   110

Glu Gln Glu Ile His Tyr Ala Arg Asp Ser Glu Thr Met Leu Ser Ile
      115   120   125

Met Ala Asn Ile Tyr Ser Asp Ile Ile Ser Pro Leu Gly Lys Lys Ile
    130   135   140

His Ile Leu Gly Ser Pro Asp Tyr Leu Arg Gln Glu Leu Val Gln Asn
145   150   155   160

Lys Ile Arg Ala Val Leu Leu Ala Gly Ile Arg Ser Ala Val Leu Trp
        165   170   175

Lys Gln Met Gly Gly Thr Lys Trp Gln Ile Leu Phe Phe Arg Arg Lys
        180   185   190

Leu Leu Ala Thr Ala Lys Gln Ile Tyr Ser Ser Ile Tyr
      195   200   205

<210> 54
<211> 203
<212> PRT
<213> Artificial

<220>
<223> Penetrating peptide consensus sequence

<400> 54

Met Ala Asn Tyr Tyr Asp Ile Thr Leu Ala Leu Ala Gly Val Cys Gln
1   5   10   15

Ala Ala Lys Leu Val Gln Gln Phe Ala His Glu Gly Gln Ala Asp Gln
        20   25   30

Ala Ala Phe Glu Thr Ser Leu Asn Thr Leu Leu Gln Ile Tyr Pro Glu
        35   40   45

Asp Thr Leu Ala Val Phe Gly Gly Lys Ala Gln Asn Leu Lys Leu Gly
    50   55   60

Leu Glu Thr Leu Leu Glu Gln Met His Gly Thr Gly Ser Asp Leu Ser
65   70   75   80

Arg Tyr Trp Ile Ser Leu Leu Ala Leu Glu Ser Lys Leu Asn Lys Asp
        85   90   95

Pro His Ala Lys Ala Glu Leu Ala Arg Arg Ile Gln Tyr Leu Pro Thr
        100   105   110

Gln Leu Glu His Tyr Asp Leu Leu Asp Glu Gln Met Leu Ser Thr Leu

```
                115                   120                   125

Ala Ser Ile Tyr Val Asp Val Ile Ser Pro Leu Gly Lys Lys Ile Gln
    130                   135                   140

Val Thr Gly Ser Thr Leu Tyr Leu Gln Gln Leu Ala Met His His Arg
145                   150                   155                   160

Ile Arg Ala Cys Leu Leu Ala Gly Ile Arg Ser Ala Val Leu Trp Arg
            165                   170                   175

Gln Val Gly Gly Thr Lys Trp Gln Val Leu Phe Ser Arg Arg Lys Ile
            180                   185                   190

Ile Ala Met Ala Lys Gln Ile Tyr Ser Ser Leu
            195                   200
```

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<210>  55
<211>  213
<212>  PRT
<213>  Artificial

<220>
<223>  Penetrating peptide consensus sequence

<400>  55
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```
Met Ala Lys Asn Tyr Tyr Asp Ile Thr Leu Ala Leu Ala Gly Ile Cys
1               5                   10                  15

Gln Ser Ala Arg Leu Val Gln Gln Leu Ala His Gln Gly His Cys Asp
            20                  25                  30

Ala Asp Ala Leu His Val Ser Leu Asn Ser Ile Ile Asp Met Asn Pro
            35                  40                  45

Ser Ser Thr Leu Ala Val Phe Gly Gly Ser Glu Ala Asn Leu Arg Val
    50                  55                  60

Gly Leu Glu Thr Leu Leu Gly Val Leu Asn Ala Ser Ser Arg Gln Gly
65                  70                  75                  80

Leu Asn Ala Glu Leu Thr Arg Tyr Thr Leu Ser Leu Met Val Leu Glu
                85                  90                  95

Arg Lys Leu Ser Ser Ala Lys Gly Ala Leu Asp Thr Leu Gly Asn Arg
            100                 105                 110

Ile Asn Gly Leu Gln Arg Gln Leu Glu His Phe Asp Leu Gln Ser Glu
            115                 120                 125
```

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```
Thr Leu Met Ser Ala Met Ala Ala Ile Tyr Val Asp Val Ile Ser Pro
    130             135         140
```

```
Leu Gly Pro Arg Ile Gln Val Thr Gly Ser Pro Ala Val Leu Gln Ser
145             150             155             160
```

```
Pro Gln Val Gln Ala Lys Val Arg Ala Thr Leu Leu Ala Gly Ile Arg
            165             170             175
```

```
Ala Ala Val Leu Trp His Gln Val Gly Gly Gly Arg Leu Gln Leu Met
            180             185             190
```

```
Phe Ser Arg Asn Arg Leu Thr Thr Gln Ala Lys Gln Ile Leu Ala His
        195             200             205
```

```
Leu Thr Pro Glu Leu
    210
```

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<210>  56
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<212>  PRT
<213>  Artificial

<220>
<223>  Penetrating peptide consensus sequence

<400>  56
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Met Ala Asn Ala Ile Tyr Asp Arg Thr Ile Ala Phe Ala Gly Ile Cys
1               5           10              15
```

```
Gln Ala Val Ala Leu Val Gln Gln Val Ala Lys Asn Gly Tyr Cys Asp
            20              25              30
```

```
Ser Asp Ala Phe Glu Thr Ser Leu Lys Ala Ile Thr Cys Thr Asn Pro
        35              40              45
```

```
Ser Asn Thr Leu Glu Val Phe Gly His Glu Ser Gln Leu Lys Leu Gly
    50              55              60
```

```
Leu Glu Cys Leu Val Lys Gly Ile Asp Ser Thr Pro Ser Gly Ser Glu
65              70              75              80
```

```
Ile Thr Arg Tyr Leu Ile Ser Leu Met Ala Leu Glu Arg Lys Leu Ser
            85              90              95
```

```
Gly Arg Arg Asp Ala Met Ser Gln Leu Gly Asp Arg Ile Gln Met Ile
            100             105             110
```

Glu Arg Gln Leu Asp His Phe Asp Leu Phe Asp Asp Gln Met Ile Ser
    115   120   125

Asn Leu Ala Ser Ile Tyr Leu Asp Val Ile Ser Pro Ile Gly Pro Arg
    130   135   140

Ile Gln Val Thr Gly Thr Pro Ala Val Leu Gln Gln Thr Ala Asn Gln
145   150   155   160

His Lys Val Arg Ala Leu Leu Leu Ser Gly Ile Arg Cys Ala Val Leu
            165   170   175

Trp Arg Gln Val Gly Gly Arg Arg Arg His Leu Ile Phe Gly Arg Lys
            180   185   190

Lys Met Ile Glu Gln Ala Gln Ile Leu Leu Ala Arg
            195   200

<210> 57
<211> 211
<212> PRT
<213> Artificial

<220>
<223> Penetrating peptide consensus sequence

<400> 57

Met Lys Lys Ile His Leu Ile Thr Leu Ser Leu Ala Gly Ile Cys Gln
1   5   10   15

Ser Ala His Leu Val Gln Gln Leu Ala Tyr Ser Gly Lys Cys Asp Ser
            20   25   30

Asn Ala Phe Ser Ile Cys Leu Lys Ser Ile Leu Glu Ile Asn Pro Thr
            35   40   45

Ser Phe Ile Ala Ile Tyr Gly Asn His Glu Lys Asn Leu Ile Ile Gly
    50   55   60

Leu Glu Ile Leu Leu Ser Thr Leu Thr Phe Ser Ser Phe Ser Tyr Ser
65   70   75   80

Tyr Ile Glu Leu Ile Lys Tyr Ile Ser Asn Met Met Ile Ile Glu Lys
            85   90   95

Lys Leu Lys Lys Ser Arg Thr Ala Ile Tyr Ser Leu Lys Asn Lys Ile
            100   105   110

```
Ser Val Ile Ser Ser Glu Tyr Tyr Leu Asn Tyr Asn Ile Lys Asn Leu
        115             120             125

Thr Arg Lys Leu Gly Glu Leu Tyr Leu Glu Ile Ile Ser Ser Leu Gly
    130             135             140

Ser Arg Ile Val Ile Lys Gly Ile Lys Asp Phe Leu Gln Asp His Gln
145             150             155             160

Ile Gln Glu Lys Ile Arg Cys Leu Leu Phe Ser Gly Ile Arg Ala Ile
            165             170             175

Val Leu Trp Lys Gln Tyr Gly Gly Asn Gln Leu Gln Leu Ile Tyr Phe
            180             185             190

Arg Tyr Phe Ile Ile Lys Lys Ala Lys Lys Ile Leu Tyr His Leu Lys
        195             200             205

Asp Ala Thr
    210
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<210>   58
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<212>   PRT
<213>   Artificial

<220>
<223>   Penetrating peptide consensus sequence

<400>   58
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Met Ser Asp Pro Arg Gln Gln Leu Ile Ala Leu Gly Ala Val Phe Glu
1               5               10              15

Ser Ala Ala Leu Val Asp Lys Leu Ala Arg Thr Gly Gln Ile Ser Glu
            20              25              30

Ala Pro Leu Gly Cys Met Leu Gly Ser Leu Leu Ala Arg Asn Pro Ala
        35              40              45

Ser Thr Leu Asp Val Tyr Gly Gly Asp Ser Leu Asn Leu Arg Asp Gly
    50              55              60

Phe Lys Ala Leu Ala Ser Ala Leu Glu Arg Lys Pro Gly Ser Leu Gln
65              70              75              80

Arg Glu Pro Leu Arg Tyr Ala Leu Ala Met Leu Thr Leu Glu Arg Gln
            85              90              95

Leu Asp Lys Arg Gly Asp Met Leu Asp Leu Ile Gly Gln Arg Leu Asp
```

100   105   110

Gln Val Glu Gln Gln Val Gln His Phe Gly Leu Val His Glu Asn Val
        115   120   125

Ile Ala Ser Phe Ala Ser Ile Tyr Gln Asp Thr Leu Ser Thr Phe Arg
    130   135   140

Gln Arg Ile Gln Val His Gly Asp Met Arg His Leu Gln Val Ser Ser
145   150   155   160

Asn Ala Ala Arg Ile Arg Ala Leu Leu Leu Ala Gly Ile Arg Ser Ala
                165   170   175

Arg Leu Trp Arg Gln Leu Gly Gly Ser Arg Trp Gln Met Val Phe Ser
                180   185   190

Arg Arg Arg Leu Leu Asn Glu Leu Tyr Pro Leu Leu Arg Gly
                195   200   205

<210>   59
<211>   204
<212>   PRT
<213>   Artificial

<220>
<223>   Penetrating peptide consensus sequence

<400>   59

Met Asn Ala Leu Ile Asp Asn Arg Val Leu Ala Leu Ala Gly Val Val
1   5   10   15

Gln Ala Leu Gln Gln Val Arg Gln Ile Ala Glu Thr Gly Gln Ser Glu
            20   25   30

Thr Ser Ala Val Arg Thr Ala Ile Asp Ser Val Leu Arg Ile Asp Ala
        35   40   45

Glu Ser Pro Glu Ala Val Tyr Gly Gly Ile Arg Asp Leu Thr Gln Gly
    50   55   60

Leu Gln Leu Leu His Asp Tyr Phe Gly Asn Gln Leu His Asp Gln Leu
65   70   75   80

Leu Pro Arg Leu Thr Leu Ala Val Leu Gln Leu Glu Arg Arg Phe Ile
                85   90   95

Arg Asp Thr Ser Ile Val Ala Ala Val Ser Ala Gly Ile Thr Gln Ala
                100   105   110

Ala His Gln Val Glu Gln Thr Gly Asp Ser Ala His Pro Glu Val Leu
    115   120   125

Ser Thr Leu Gly Ala Leu Tyr Ala Asn Thr Ile Ser His Leu Arg Pro
    130   135   140

Arg Ile Ile Val Gln Gly Asn Pro His Tyr Leu Gly Gln Ala Gly Val
145   150   155   160

Val Ala Glu Ile Arg Ala Met Leu Leu Ala Ala Leu Arg Ser Ala Val
         165   170   175

Leu Trp Arg Gln Leu Asn Gly Asn Leu Leu Asp Phe Leu Leu Ala Lys
        180   185   190

Arg Ala Met Ala Ala Ala Thr Glu Arg Ala Leu Arg
        195   200

<210> 60
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<212> PRT
<213> Artificial

<220>
<223> Fully conserved "strong" amino acid residue chain

<400> 60

Asn Arg Glu Gln Lys
1   5

<210> 61
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "strong" amino acid residue chain

<400> 61

Asn His Gln Lys
1

<210> 62
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "strong" amino acid residue chain

<400> 62

Asn Asp Glu Gln
1

<210> 63
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "strong" amino acid residue chain

<400> 63

Gln His Arg Lys
1

<210> 64
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "strong" amino acid residue chain

<400> 64

Met Ile Leu Val
1

<210> 65
<211> 4
<212> PRT
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<220>
<223> Fully conserved "strong" amino acid residue chain

<400> 65

Met Ile Leu Phe
1

<210> 66
<211> 4
<212> PRT
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<220>
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<400> 66

Ser Thr Asn Lys
1

<210> 67
<211> 4

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<212> PRT
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<220>
<223> Fully conserved "weak" amino acid residue chain

<400> 67

Ser Thr Pro Ala
1


<210> 68
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "weak" amino acid residue chain

<400> 68

Ser Gly Asn Asp
1


<210> 69
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "weak" amino acid residue chain

<400> 69

Ser Asn Asp Glu Gln Lys
1               5


<210> 70
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "weak" amino acid residue chain

<400> 70

Asn Asp Glu Gln His Lys
1               5


<210> 71
<211> 6
<212> PRT
<213> Artificial

<220>
<223> Fully conserved "weak" amino acid residue chain

<400> 71
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Asn Glu Gln His Arg Lys
1   5

<210> 72
<211> 23
<212> PRT
<213> Bacillus subtilis

<400> 72

Asn Leu Thr Lys Thr Ser Leu Leu Leu Ala Gly Leu Cys Thr Ala Ala
1   5   10   15

Gln Met Val Phe Val Thr His
              20